WHAT IS CLAIMED IS:

1. A method of designing a nucleic acid probe array to target a transcript cluster comprising:

selecting a first set of probes comprising at least one probe targeting a first region

5 immediately upstream of a first polyadenylation site in the transcript cluster; and

selecting a second set of probes comprising at least one probe targeting a second

region immediately upstream of a second polyadenylation site in the transcript cluster,

wherein the first and second regions are different.

2. The method of Claim 1 wherein the first and second polyadenylation sites are

10 alternative polyadenylation sites.

3. The method of Claim 2 wherein the first polyadenylation site is a putative

polyadenylation site.

4. The method of Claim 1 wherein the first region is within 800 bases upstream of the

first polyadenylation site and the second region is within 800 bases upstream of the

15 second polyadenylation site.

5. The method of Claim 4 wherein the first region is within 600 bases upstream of the

first polyadenylation site and the second region is within 600 bases upstream of the

second polyadenylation site.

6. The method of Claim 5 wherein the target nucleic acid represents a cluster of

20 transcript sequences including RNA and ESTs.

7. The method of Claim 6 wherein the first polyadenylation site is in a full length

mRNA and the first set of probes are selected to target the full length mRNA as an

exemplar sequence of the cluster.

8. The method of Claim 6 wherein the first polyadenylation site is shared by a stack of sequences in the cluster and the probe are selected to target the consensus sequence of the cluster, wherein the stack of sequences comprises at least 2 sequences.

9. The method of Claim 8 wherein the stack of sequences comprises at least 5 sequences.

10. The method of Claim 9 wherein the stack of sequences comprises at least 8 sequences.

11. The method of Claim 7, 8, 9, or 10 wherein the first and second probe sets comprises at least 5 probes.

12. The method of Claim 11 wherein the first and second probe sets comprises at least 10 probes.

13. A nucleic acid probe array comprising a first set of probes comprising at least one probe targeting a first region immediately upstream of a first polyadenylation site in a transcript cluster; and a second set of probes comprising at least one probe targeting a second region immediately upstream of a second polyadenylation site in the transcript cluster, wherein the first and second regions are different.

14. The array of Claim 13 wherein the first and second polyadenylation sites are alternative polyadenylation sites.

15. The array of Claim 14 wherein the first polyadenylation site is a putative polyadenylation site.

16. The array of Claim 13 wherein the first region is within 800 bases upstream of the first polyadenylation site and the second region is within 800 bases upstream of the second polyadenylation site.

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17. The array of Claim 16 wherein the first region is within 600 bases upstream of the first polyadenylation site and the second region is within 600 bases upstream of the second polyadenylation site.

18. The array of Claim 17 wherein the target nucleic acid represents a cluster of transcript sequences including RNA and ESTs.

19. The array of Claim 18 wherein the first polyadenylation site is in a full length mRNA and the first set of probes are selected to target the full length mRNA as an exemplar sequence of the cluster.

20. The array of Claim 19 wherein the first polyadenylation site is shared by a stack of sequences in the cluster and the probe are selected to target the consensus sequence of the cluster, wherein the stack of sequences comprises at least 2 sequences.

21. The array of Claim 20 wherein the stack of sequences comprises at least 5 sequences.

22. The array of Claim 21 wherein the stack of sequences comprises at least 8 sequences.

23. The array of Claim 19, 20, 21, or 22 wherein the first and second probe sets comprises at least 5 probes.

24. The array of Claim 23 wherein the first and second probe sets comprises at least 10 probes.

25. The array of Claim 23 wherein the probes are immobilized at a density greater than 400 different probes $/cm^2$.

26. The array of Claim 23 wherein the probes are immobilized at a density greater than 1000 different probes $/cm^2$.

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